



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Conti-Fine, B.M.

(ii) TITLE OF INVENTION: PREVENTION OF EXPERIMENTAL MYASTHANIA GRAVIS BY NASAL ADMINISTRATION OF SYNTHETIC T EPITOPE SEQUENCES

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.

(B) STREET: 121 South Eighth Street, 1600 TCF Tower

(C) CITY: Minneapolis

(D) STATE: MN

(E) COUNTRY: USA

(F) ZIP: 55402

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette

(B) COMPUTER: IBM Compatible

(C) OPERATING SYSTEM: Windows 95

(D) SOFTWARE: FastSEQ for Windows Version 2.0b

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/991,143

(B) FILING DATE: 16-DEC-1997

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Embretson, Janet E

(B) REGISTRATION NUMBER: 39,665

(C) REFERENCE/DOCKET NUMBER: 600.423US1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 612-373-6959

(B) TELEFAX: 612-339-3061

(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1667 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAGCACAGGC CACCACTCTG CCCTGGTCCA CACAAGCTCC GGTAGCCCAT GGAGCCCTGG 60
 CCTCTCCTCC TGCTCTTTAG CCTTGCTCA GCTGGCCTCG TCCTGGGCTC CGAACATGAG 120
 ACCCGTCTGG TGGCAAAGCT ATTTAAAGAC TACAGCAGCG TGGTGCGGCC AGTGGAAAGAC 180
 CACCGCCAGG TCGTGGAGGT CACCGTGGGC CTGAGCTGA TACAGCTCAT CAATGTGGAT 240
 GAAGTAAATC AGATCGTGAC AACCAATGTG CGTCTGAAAC AGCAATGGGT GGATTACAAC 300
 CTAAAATGGA ATCCAGATGA CTATGGCGGT GTGAAAAAAA TTCACATTCC TTCAGAAAAG 360
 ATCTGGCGCC CAGACCTTGT TCTCTATAAC AATGCAGATG GTGACTTTGC TATTGTCAAG 420
 TTCACCAAAG TGCTCCTGCA GTACACTGGC CACATCACGT GGACACCTCC AGCCATCTTT 480
 AAAAGCTACT GTGAGATCAT CGTCACCCAC TTTCCCTTG ATGAACAGAA CTGCAGCATG 540
 AAGCTGGCA CCTGGACCTA CGACGGCTCT GTCGTGGCCA TCAACCCGGA AAGCGACCAG 600
 CCAGACCTGA GCAACTTCAT GGAGAGCGGG GAGTGGGTGA TCAAGGAGTC CGGGGGCTGG 660
 AAGCACTCCG TGACCTATTCTG CTGCTGCCCT GACACCCCT ACCTGGACAT CACTTACAC 720
 TTCTGTCTGC AGCGCTGCTC CCTCTACTTC ATCGTCAACG TCATCATCCC CTGCCTGCTC 780
 TTCTCCTTCT TAATCTGGCT GGTATTCTAC CTGCCCCACAG ACTCAGGGGA GAAGATGACT 840
 CTGAGCATCT CTGCTTTACT GTCTTGTACT GTGTTCTTC TGGTCATCGT GGAGCTGATC 900
 CCCTCCACGT CCAGTGCTGT GCCCTTGATT GGAAAATACA TGCTGTTCAC CATGGTGTTC 960
 GTCATTGCT CCATCATCAT CACTGTGATC GTCATCAACA CACACCACCG CTCACCCAGC 1020
 ACCCATGTCA TGCCCAACTG GGTGCGGAAG GTTTTATCG ACACTATCCC AAATATCATG 1080
 TTTTCTCCA CAATGAAAAG ACCATCCAGA GAAAAGCAAG ACAAAAAGAT TTTTACAGAA 1140
 GACATTGATA TCTCTGACAT TTCTGGAAAG CCAGGGCCTC CACCCATGGG CTTCCACTCT 1200
 CCCCTGATCA AACACCCCGA GGTGAAAAGT GCCATCGAGG GCATCAAGTA CATCGCAGAG 1260
 ACCATGAAGT CAGACCAGGA GTCTAACAAAT GCGGCGGGCAG AGTGGAAAGTA CGTTGCAATG 1320
 GTGATGGACC ACATACTCCT CGGAGTCTTC ATGTTGTTT GCATCATCGG AACCTAGCC 1380
 GTGTTTGAG GTCGACTCAT TGAATTAAAT CAGCAAGGAT GAGCAGAAAA TGAGCTGAGC 1440
 TTAGCTCTGC CCTGGAACCT ACCAGAGCAG AGAAGGGCAG GAGAGGAAGA TTTGTCTACT 1500
 TGCTCCACTC GCACTTATCA AACGTGTTAT ATTCCATACT TATTATTGAT GATAAGATTT 1560
 ACCTTTATGT AAGTTTATGG CCTTGAAGTG TTTCTATATT GCTTCTCCCT TTAGTTCTGC 1620
 TGTCTCCCTG AAGAGTGAAC CCTCTTAGT AAATGAAACT AATCACT 1667

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 457 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Glu	Pro	Trp	Pro	Leu	Leu	Leu	Leu	Phe	Ser	Leu	Cys	Ser	Ala	Gly
1					5				10				15		
Leu	Val	Leu	Gly	Ser	Glu	His	Glu	Thr	Arg	Leu	Val	Ala	Lys	Leu	Phe
					20			25				30			
Lys	Asp	Tyr	Ser	Ser	Val	Val	Arg	Pro	Val	Glu	Asp	His	Arg	Gln	Val
					35			40				45			

Val Glu Val Thr Val Gly Leu Gln Leu Ile Gln Leu Ile Asn Val Asp
50 55 60
Glu Val Asn Gln Ile Val Thr Thr Asn Val Arg Leu Lys Gln Gln Trp
65 70 75 80
Val Asp Tyr Asn Leu Lys Trp Asn Pro Asp Asp Tyr Gly Gly Val Lys
85 90 95
Lys Ile His Ile Pro Ser Glu Lys Ile Trp Arg Pro Asp Leu Val Leu
100 105 110
Tyr Asn Asn Ala Asp Gly Asp Phe Ala Ile Val Lys Phe Thr Lys Val
115 120 125
Leu Leu Gln Tyr Thr Gly His Ile Thr Trp Thr Pro Pro Ala Ile Phe
130 135 140
Lys Ser Tyr Cys Glu Ile Ile Val Thr His Phe Pro Phe Asp Glu Gln
145 150 155 160
Asn Cys Ser Met Lys Leu Gly Thr Trp Thr Tyr Asp Gly Ser Val Val
165 170 175
Ala Ile Asn Pro Glu Ser Asp Gln Pro Asp Leu Ser Asn Phe Met Glu
180 185 190
Ser Gly Glu Trp Val Ile Lys Glu Ser Arg Gly Trp Lys His Ser Val
195 200 205
Thr Tyr Ser Cys Cys Pro Asp Thr Pro Tyr Leu Asp Ile Thr Tyr His
210 215 220
Phe Val Met Gln Arg Leu Pro Leu Tyr Phe Ile Val Asn Val Ile Ile
225 230 235 240
Pro Cys Leu Leu Phe Ser Phe Leu Thr Gly Leu Val Phe Tyr Leu Pro
245 250 255
Thr Asp Ser Gly Glu Lys Met Thr Leu Ser Ile Ser Val Leu Leu Ser
260 265 270
Leu Thr Val Phe Leu Leu Val Ile Val Glu Leu Ile Pro Ser Thr Ser
275 280 285
Ser Ala Val Pro Leu Ile Gly Lys Tyr Met Leu Phe Thr Met Val Phe
290 295 300
Val Ile Ala Ser Ile Ile Thr Val Ile Val Ile Asn Thr His His
305 310 315 320
Arg Ser Pro Ser Thr His Val Met Pro Asn Trp Val Arg Lys Val Phe
325 330 335
Ile Asp Thr Ile Pro Asn Ile Met Phe Phe Ser Thr Met Lys Arg Pro
340 345 350
Ser Arg Glu Lys Gln Asp Lys Lys Ile Phe Thr Glu Asp Ile Asp Ile
355 360 365
Ser Asp Ile Ser Gly Lys Pro Gly Pro Pro Pro Met Gly Phe His Ser
370 375 380
Pro Leu Ile Lys His Pro Glu Val Lys Ser Ala Ile Glu Gly Ile Lys
385 390 395 400
Tyr Ile Ala Glu Thr Met Lys Ser Asp Gln Glu Ser Asn Asn Ala Ala
405 410 415
Ala Glu Trp Lys Tyr Val Ala Met Val Met Asp His Ile Leu Leu Gly
420 425 430
Val Phe Met Leu Val Cys Ile Ile Gly Thr Leu Ala Val Phe Ala Gly
435 440 445
Arg Leu Ile Glu Leu Asn Gln Gln Gly
450 455